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## RAW SEQUENCE LISTING

DATE: 07/09/2003

PATENT APPLICATION: US/09/830,111D

TIME: 09:22:53

Input Set : A:\21581-265.seq.ST25.txt

Output Set: N:\CRF4\07092003\I830111D.raw

3 <110> APPLICANT: Kaneka Corporation  
 4 Matsuda, Hideyuki  
 5 Kawamukai, Makoto  
 6 Yajima, Kazuyoshi  
 7 Ikenaka, Yasuhiro  
 8 Hasegawa, Junzo  
 9 Takahashi, Satomi  
 11 <120> TITLE OF INVENTION: Process For Producing Coenzyme Q10  
 13 <130> FILE REFERENCE: 21581-00265-US  
 15 <140> CURRENT APPLICATION NUMBER: 09/830,111D  
 16 <141> CURRENT FILING DATE: 2001-07-23  
 18 <160> NUMBER OF SEQ ID NOS: 2  
 20 <170> SOFTWARE: PatentIn version 3.2  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 1653  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Saioella complicata  
 27 <400> SEQUENCE: 1

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32	aaatccatat	accatggcct	caccagcact	gcggatacga	agcatcagct	ctcgatcaat	180
34	cgcctctctg	cgatcggtta	ccctaagaac	agcctcggca	ccttcattac	gactaagatg	240
36	taccccgacg	agccggccat	cgagttcatg	ggctgctgct	gtgtcttcgg	cgtcgagact	300
38	ggttgagcct	gatccgaatc	aacctctcat	caatccgctc	aacttggtcg	gtcccagat	360
40	gtcaaatctt	acatccaaca	tccgatctct	cctcggttca	ggacaccctt	ctctcgacac	420
42	tgtcgctaaa	tactatgttc	agtctgaggg	aaagcatatt	cgtccgctca	tggtactgct	480
44	gatggctcag	gcgacggagg	ttgcgcaaaa	agttcagggt	tgggagaagg	tcgtggaggt	540
46	tccggtgaac	gagggactcg	caccaccaga	ggtgctcaat	gacaagaacc	cagatatgat	600
48	gaacatgagg	tcaggaccat	taacgaagga	cggcgagatc	gagggacaga	cgtcgaatat	660
50	cctcgccctg	caacggcggt	tggtgagat	cacggagatg	atccatgcag	catcactcct	720
52	ccacgacgac	gttatcgacg	cttcgagac	cagacgaaac	gcaccatccg	gaaaccaggc	780
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56	attggcgagg	ttgcgcaatc	cggaggtgat	tgagcttttg	gctactgtta	ttgcaaaactt	900
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60	gacgcaggaa	acgttcgatt	actattttgca	gaagacttac	ttgaagactg	cgtccttgat	1020
62	tgccaagtcg	tgacagagca	gtgcgcttct	gggtggtgct	acgcctgagg	ttgctgatgc	1080
64	tgcttatgct	tacggaagga	accttggttt	ggcattccag	atcgtcgacg	acatgctcga	1140
66	ctacaccgtc	tccgctaccg	acctcggtaa	gcccgcgggt	gcagacctcc	agctcggctc	1200
68	cgccaccgcg	ccggccctct	tcgcatggaa	gcaccacgcc	gagctcggtc	ccatgatcaa	1260
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72	tggattggag	aagacgagag	ccttggcgga	ggagtatgcc	cagaaggcgt	tggatgcaat	1380
74	tcggacgttc	ccggagagtc	cggcacggaa	ggctttggag	cagttgacgg	acaaggtggt	1440
76	gactaggtca	agataggaat	tcgagctcgg	tacccgggga	tcctctagag	tcgacctgca	1500

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78 ggcatgcaag cttggctgtt ttggcggatg agagaagatt ttcagcctga tacagattaa 1560
80 atcagaacgc agaagcggtc tgataaaaca gaatttgcct ggcggcagta gcgcggtggt 1620
82 cccacctgac cccatgccga actcagaagt gaa 1653
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96 Ala Ser Leu Arg Ser Val Thr Leu Arg Thr Ala Ser Ala Pro Ser Leu
97 20 25 30
100 Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro Ser Ser Ser Trp Ala Ala
101 35 40 45
104 Ala Val Ser Ser Ala Ser Arg Leu Val Glu Pro Asp Pro Asn Gln Pro
105 50 55 60
108 Leu Ile Asn Pro Leu Asn Leu Val Gly Pro Glu Met Ser Asn Leu Thr
109 65 70 75 80
112 Ser Asn Ile Arg Ser Leu Leu Gly Ser Gly His Pro Ser Leu Asp Thr
113 85 90 95
116 Val Ala Lys Tyr Tyr Val Gln Ser Glu Gly Lys His Ile Arg Pro Leu
117 100 105 110
120 Met Val Leu Leu Met Ala Gln Ala Thr Glu Val Ala Pro Lys Val Gln
121 115 120 125
124 Gly Trp Glu Lys Val Val Glu Val Pro Val Asn Glu Gly Leu Ala Pro
125 130 135 140
128 Pro Glu Val Leu Asn Asp Lys Asn Pro Asp Met Met Asn Met Arg Ser
129 145 150 155 160
132 Gly Pro Leu Thr Lys Asp Gly Glu Ile Glu Gly Gln Thr Ser Asn Ile
133 165 170 175
136 Leu Ala Ser Gln Arg Arg Leu Ala Glu Ile Thr Glu Met Ile His Ala
137 180 185 190
140 Ala Ser Leu Leu His Asp Asp Val Ile Asp Ala Ser Glu Thr Arg Arg
141 195 200 205
144 Asn Ala Pro Ser Gly Asn Gln Ala Phe Gly Asn Lys Met Ala Ile Leu
145 210 215 220
148 Ala Gly Asp Phe Leu Leu Gly Arg Ala Ser Val Ala Leu Ala Arg Leu
149 225 230 235 240
152 Arg Asn Pro Glu Val Ile Glu Leu Leu Ala Thr Val Ile Ala Asn Leu
153 245 250 255
156 Val Glu Gly Glu Phe Met Gln Leu Lys Asn Thr Val Asp Asp Ala Ile
157 260 265 270
160 Glu Ala Thr Ala Thr Gln Glu Thr Phe Asp Tyr Tyr Leu Gln Lys Thr
161 275 280 285
164 Tyr Leu Lys Thr Ala Ser Leu Ile Ala Lys Ser Cys Arg Ala Ser Ala
165 290 295 300
168 Leu Leu Gly Gly Ala Thr Pro Glu Val Ala Asp Ala Ala Tyr Ala Tyr
169 305 310 315 320
172 Gly Arg Asn Leu Gly Leu Ala Phe Gln Ile Val Asp Asp Met Leu Asp

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176 Tyr Thr Val Ser Ala Thr Asp Leu Gly Lys Pro Ala Gly Ala Asp Leu
177           340           345           350
180 Gln Leu Gly Leu Ala Thr Ala Pro Ala Leu Phe Ala Trp Lys His His
181           355           360           365
184 Ala Glu Leu Gly Pro Met Ile Lys Arg Lys Phe Ser Asp Pro Gly Asp
185           370           375           380
188 Val Glu Arg Ala Arg Glu Leu Val Glu Lys Ser Asp Gly Leu Glu Lys
189 385           390           395           400
192 Thr Arg Ala Leu Ala Glu Glu Tyr Ala Gln Lys Ala Leu Asp Ala Ile
193           405           410           415
196 Arg Thr Phe Pro Glu Ser Pro Ala Arg Lys Ala Leu Glu Gln Leu Thr
197           420           425           430
200 Asp Lys Val Leu Thr Arg Ser Arg
201           435           440

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**VERIFICATION SUMMARY**

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